

SEQID NO: 1

 ${\it /translation = "MGSVLSTDSGKSAPASATARALERRRDPELPVTSFDCAVCLEVL}$

 $\label{thm:linear} HQPVRTRCGHVFCRSCIATSLKNNKWTCPYCRAYLPSEGVPATDVAKRMKSEY\\ KNCAE$

 ${\tt CDTLVCLSEMRAHIRTCQKYIDKYGPLQELEETAARCVCPFCQRELYEDSLLDHC} \\ {\tt ITH}$

HRSERRPVFCPLCRLIPDENPSSFSGNLIRHLQVSHTLFYDDFIDFNIIEEALIRRVL DRSLLEYVNHSNTT"



SEQ ID NO: 2

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Figure C

l acttetgaca gtggggaaag cagetgtgtg tgatagettg gaaggtttae tgetgeetea 61 agtectette tetgeagttg aggttteagg ttteaateet eccaatacea eaagaeagag 121 cacggggcgg etgeegeete egeeteegeg eettaaceta ggeggettge egaagatete 181 ageccegegg eegegegete geeetgeeet agaccagggt tgggegeage ggeggaggtg 241 gettetggge tgegegaget gggagagetg ggaggeggeg ategeagetg ggeegggaet 301 teetteetee aeegeaegge aacaaaacaa eeetgeggea ggeaetgagt gettegeage 361 tgtctgggcg agaggcacag cgatgggctc cgtgctgagc accgacagcg gcaaatcggc 421 georgeetet gecaeegege gggeeetgga gegeaggagg gaeeeggagt tgeeegteae 481 gtccttcgac tgcgccgtgt gccttgaggt gttacaccag cctgtccgga cccgctgcgg 541 ccacgtatte tgeegtteet gtattgetae eagtetgaag aacaacaagt ggaeetgtee 601 ttattgccgg gcatatette etteagaagg agtteeagea aetgatgtag eeaaaagaat 661 gaaatcagag tataagaact gegetgagtg tgacaccetg gtttgeetea gtgaaatgag 721 ggcacatatt eggacttgte agaagtacat agataagtat ggaccactae aagaacttga 781 ggagacagca gcaaggtgtg tatgtccctt ttgtcagagg gaactgtatg aagacagctt 841 getggateat tgtattacte ateacagate ggaacggagg cetgtgttet gtecaetttg 901 cogtttaata cocgatgaga atccaagcag cttcagcggc aatttaataa gacatetgca 961 agttagtcac actttgtttt atgatgattt catagatttt aatataattg aggaagctct 1021 tateegaaga gtettagaee ggteaettet tgaatatgtg aateaetega acaecacata 1081 attitattaa aacgaaggga aaagggacca ctgaattgca ccatttaaga tgctgcttga

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SEQID NO. 4

Figure 1 D

181 ageccegege eegegegete geettgeet agaceaggt tgggegeage ggeggaggtg
241 gettetggge tgegegaget gggagagetg ggaggegeg ategeagetg ggeegggact
301 teetteete acegeaegge aacaaaacaa eettgeggea ggeaetgagt gettegeage
361 tgtetggge agaggeaeag egatgggete egtgetgage acegacageg geaaategge
421 geeegeetet geeaeegge gggeeetgga gegeaggagg gaeeeggagt tgeeegteae
481 gteettegae tgegeegtgt geettgaggt gttacaceag eetgteegga eeegetgegg
541 ceaegtatte tgeegtteet gtattgetae eagtetgaag aacaacaagt ggaeetgtee
601 ttattgeegg geatatette etteagaagg agtteeagea actgatgtag eeaaaagaat
661 gaaateagag tataagaaet gegetgagtg tgacaceetg gtttgeetea gtgaaatgag
721 ggeaeatatt eggaettgte agaagtaeat agataagtat ggaeeactae aagaaettga
781 ggagacagea geaaggtgtg tatgteeett ttgteagagg gaaetgtatg aagacaget

841 getggateat tgtattaete ateacagate ggaaeggagg cetgtgttet g



TRAC1 genomic region:

SEQID NO:5

atttttagataatattaaggatttggaatttaatcctaaggattaggaga gctattaaaggattttgtgcatggggtgacacaagatgtttgcttttcaa aagatcactttagttgccatgtggataataaactggagagaggcaatgat ggatgcgggtagagcagttaggaactactgccattaagtcacacaagaga atgcagtgatttaaaataagcggtggctatggaaatagaagaaaatgagc gatcatgaggtcaggagttcacgactagcctggccaacatggtgaaactc cgtctctaccaaaaatataataaaaattagccgggtgtggtggcatgcgcc tgcaatcccagctactcaggaggctgaggcaggagaatcacttgaaccca ggaggcagaggttgcagtgagctgagattgcgccactgcacacttccagc ctgggcgacagagagagacttcatctcagaaaaaaaaagaactactgagat a cat att gg agg cagg att gt gat tat gctt gat tca at gt ga at ga gg aagaggaagaaatcaaggatgacttccaggtgtctagactgagctataaag tggatcatagtgccatttgctaaaagagagatcaaccactggaggaggct gctactata at gagttcatt at tggagac at tgggctgagggtgtt tat gt caa at g g t cag t cat g t a a g c t at t g g a c at t t g a at g g c ctggggtagagataaagatgtgaaagtttttggaaccgaaatagtgacaga gaagggaaaaggtcctaagacagaatcctaggatctccagcccagagcca gagggaaagtcagagtgtttccagaaggaggggatggtcagcactaacaa a catagtt g aggggt caag caaaaaaaaa tagct gaaaagaat ctatt g g aattagttacatgaacgtcaccagtgacactgataataaagcagtttttgg acagatggaggtggagaggttggttcagaacccagactggactgaataag a agtgaata atta agaa atgatgacaa a atgtag aggat cagatca agagatttggccttgaagcggatatggggcaggagttgaggcataagtgggatg aaagggaggtttttgttttccttttgaagatgggaataactaccttttca tcttatttccccccccaccgcctgcccccaccaccatgctccagct $ccatagg tott {\color{blue}tctt} ctttcttt {\color{blue}tg} {\color{blue}tctg} {\color{blue}cct} {\color{blu$ acgctttttcctaaatctttgaatggctcacttcttttcattattcatgg ctctgctcaaatgtcacttcatccaaaaattcttctctgagcttattctt $ctcctc attgccatttactgttttatcttcttcatggctctg \\ attatctg$ a a at gatttt gtt cattt gtt tat ggatt gatta cat gt at ctt ccttttgtttgtttgttttttgagacagagtctcgctctgttacccacgatgga gtgtagtggcatggtctcggctcactgcaacctccacctcttgggtgcaa gtggttctcctgcctcagcctccaagtagctgggactacacgcatgtgc caccacactggctaatttttgtatttttagtacaaaaatttttactaaa gaa at gt at ttc tagt ag ag ac gg gg tt tc act at gt tg gc cag gc tg gtcttgaactcctgaccttgtgatccacctgcctcggcctcccaaattgctg ggatttcaggcgtgagccactgcacccagcctgttttggtttttgagac agggtetecetetgttgeceaggetggagtgeagtggeatgatetegget cactgeagecteeacettteeggtteaagegattettgtgeeteagecte ccaagtagctcacacccagctaagttttgtatttttagtagagacagggt

Figure ont'ol

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SEQ NO:5 Contid

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Figure 1 E cont'al

SEQ NO:5 contid



SEQ ID NO: 6

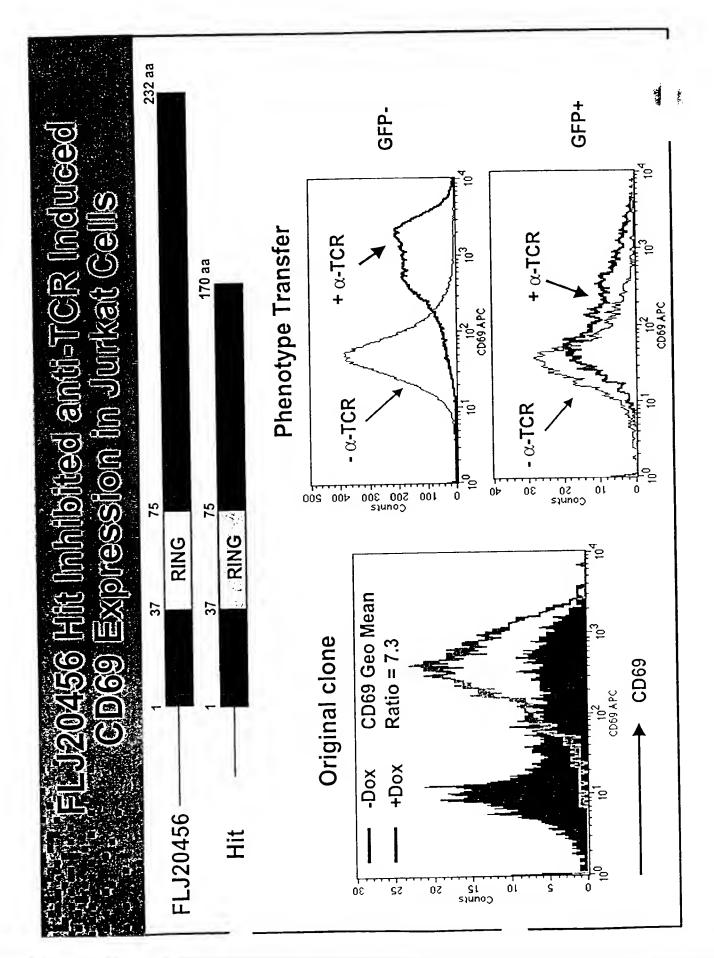
Mouse TRAC1 cDNA sequence:

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Mouse TRAC1 protein (3rd frame)

SEQ ID NO: 7

SAXXGSLLSSDSSKSAPASATPRTLERSGDSELPITSFDCSVCLEVLHQP
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ELDEDCLLDHCIIHHRSERRPVFCPLCHSRPDESPSTFNGSLIRHLQVSH
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ion in Jurkat Cells Does Not Inh

232 aa

75

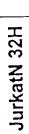
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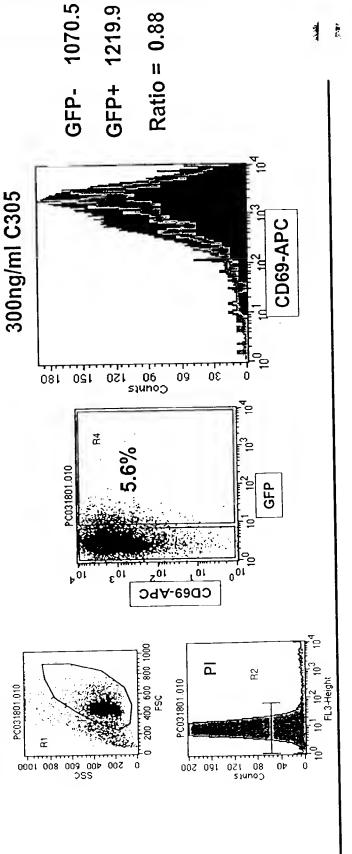
RING

FLJ20456

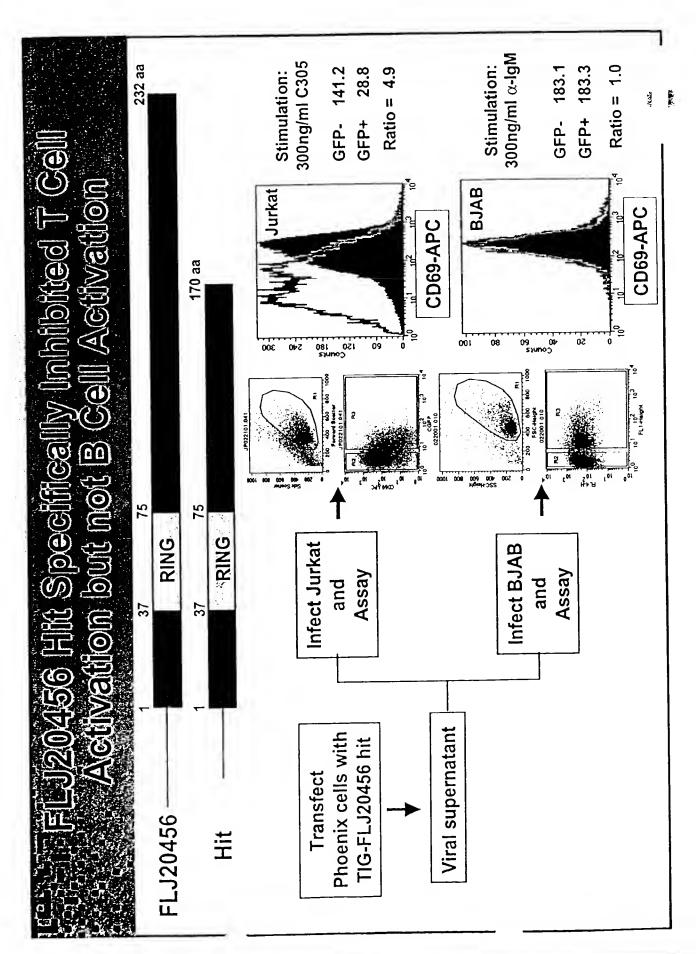
Pfu PCR product amplified from a capped human brain cDNA library.

One N to S polymorphism with FLJ20456 NM_017831.1 at amino acid 186, present in EST database.



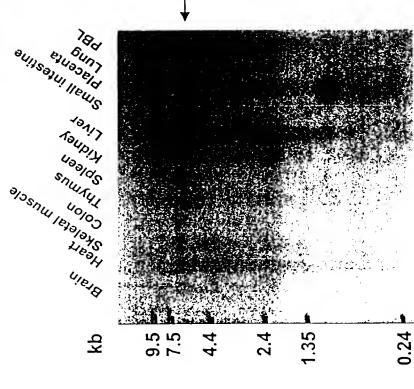






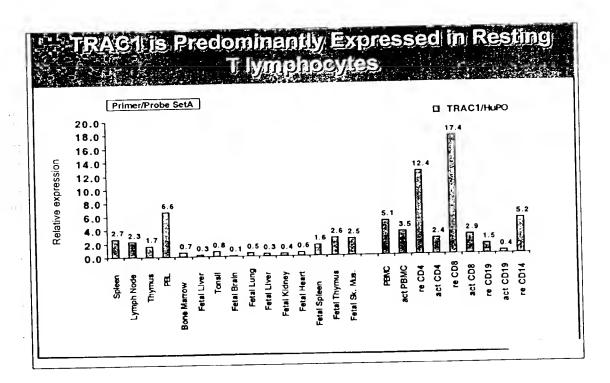
etic Organs 456 IS Stroi

170 aa RING 37 Probe: FLJ20456 Hit



←— FLJ20456

- FLJ20456 is expressed in multiple tissues
 - The strongest expression is in PBL, Liver and Spleen



FILZO456 Sequence is Most Similar to Two Sequences
Ring domain
Consensus #1
FLZ20456.ppp MG S V L S T D S G K S A P A S A T A R A L E R R R D P E L P V T S F D C A V C L E V L H O P V R - TIR C G H V F C I A T S L K N 67 ZEF313.ppp
Consensus #1 C C R
E.720456. pap NKWTCEYCR AYLPSE GVRATDVAKRMKSEYKNCAEGDTLVCLSOMRAHIRTGOKYIDKYGPLOE 131 zmf313. pap KKPVGGVCR SALAP GVRAVELEROIESTETSCHGCRKNFFLSKIRSHVATCSKYON - YIMEGV 121 STRIN pap SGAHCELCRGNVTRRERACPERALDLENIMRKFSGSCRCCAKOIKFYRMRHHYKSCKKYODEYGVSSI 117
Consensus #1
FLIZO456.pep LEETAAR
Consensus #1 . V . C P . C P P
FLZ20456.ppg PVFCPLCRLIPDENPSSFSGNLIRHLGVSHTLFYDDFLDFNIIBEALIRRVLDRSLLEYUNHSNTT. 233 zmf313.ppg SVVCPICASMPWGDPNYRSANFREHILDRRHRSYDTFVDYDVDEEDMMNQVLQRSIIDQ. 229 SRRN.ppg PVTCPICVSLPWGDPSQITRNEVSHINGRRQEDYGEFVNLQLDEETQYQTAVEESFQVNI. 246

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	FLJ20456.pep	znf313.pep	STRIN.pep	
	-	2	3	
3	22.3	27.9		3
2	26.6		134.7	2
٦		130.4	140.9 134.7	1
	-	2	3	
divergence				

Percent Identity

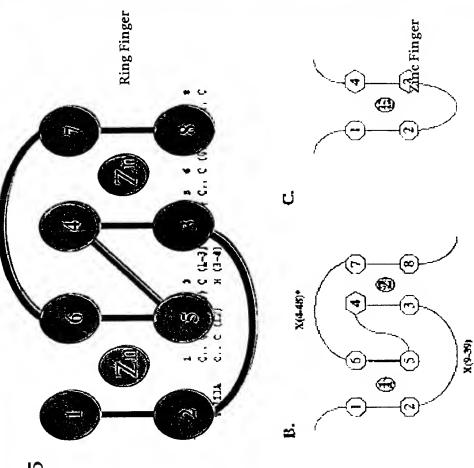
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RING Anger vs. Zinc Anger proteins

Ring-HC: $C_3HC_4 = Cys$ in position 5 Ring H2: $C_3H2C_3 = His$ in position 5

- Ring finger domains have a conserved pattern of Cys and His residues that coordinate two zinc atoms to form a cross-brace structure
- Ring fingers are structurally distinct from zinc fingers



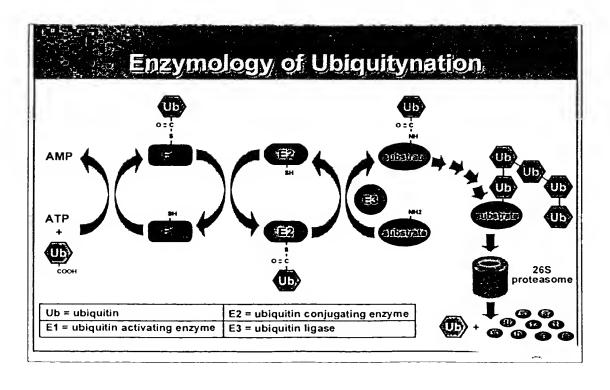


Ubiquitin Pathway Components

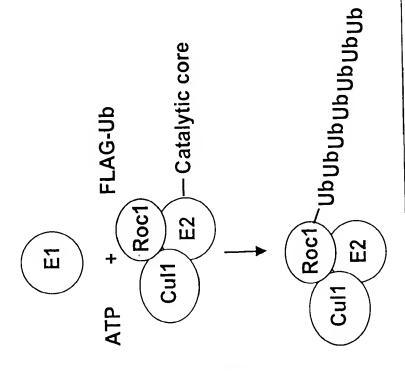
- E1: ubiquitin-activating enzyme, with a major isoform that may work broadly
- E2: ubiquitin-conjugating enzyme, a class of ~14 enzymes, interacts with E3
- E3: ubiquitin ligases, a broad and growing group of activities that promote addition of ubiquitin to specific proteins
- Proteasome-a 26S complex containing a 19S lid and base that mediates ATP- and ubiquitin-chain-dependent binding of substrates and a 20S catalytic core with three known proteolytic activities.

10 A

10B



A Reconstituted, Substrate-independent Assay for Studying Ligase Catalysis



The substrate-independent reaction has the same catalytic properties and requirements for Roc1/Cul1 as the substrate-dependent reaction

Reaction Components

Ή.

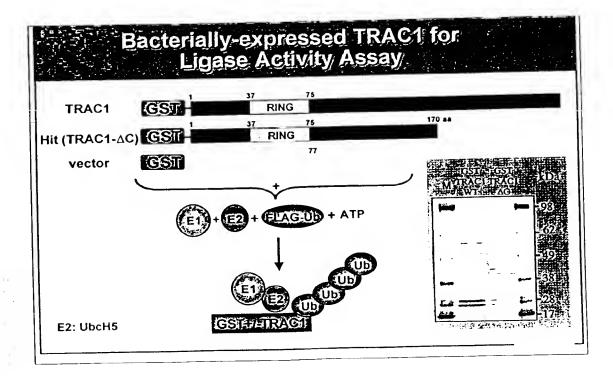
E2 (UbcH5): GST-fusion (cleaved), E. coli

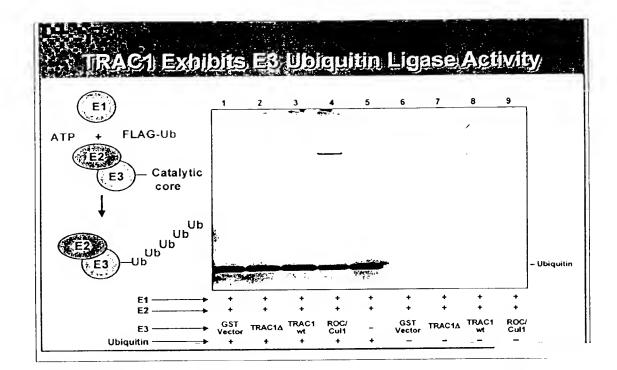
E3 (Ring/cullin): His-tagged, coexpressed, baculovirus

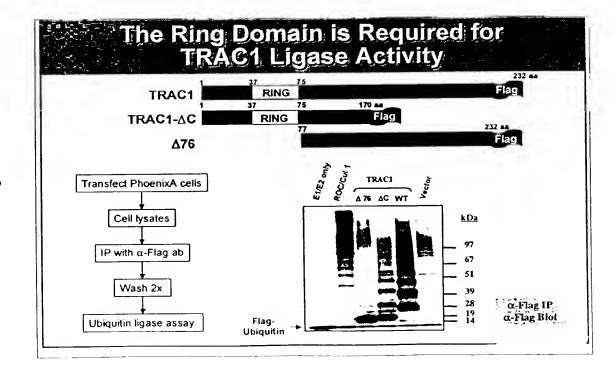
Ubiquitin: FLAG-tagged, E. coli



Figure 11 B



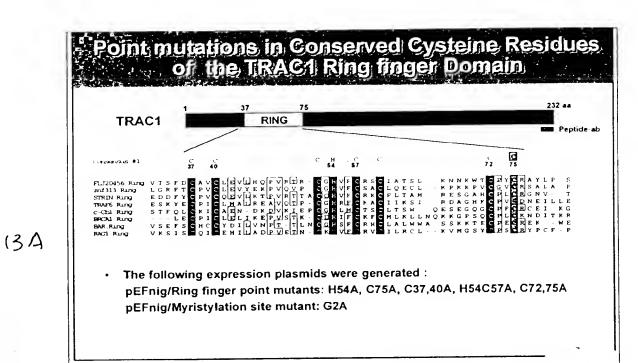


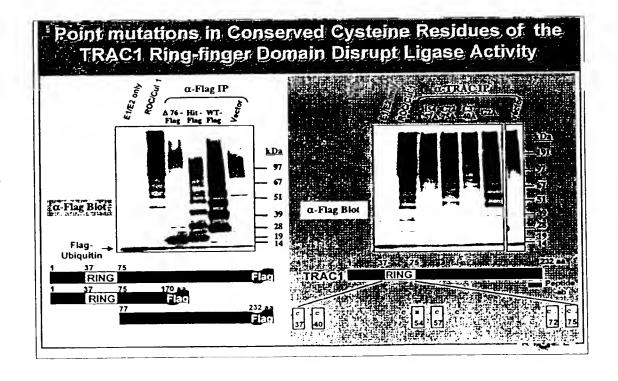


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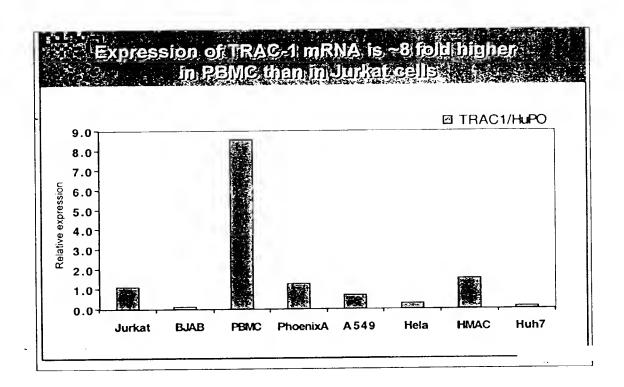
12 B

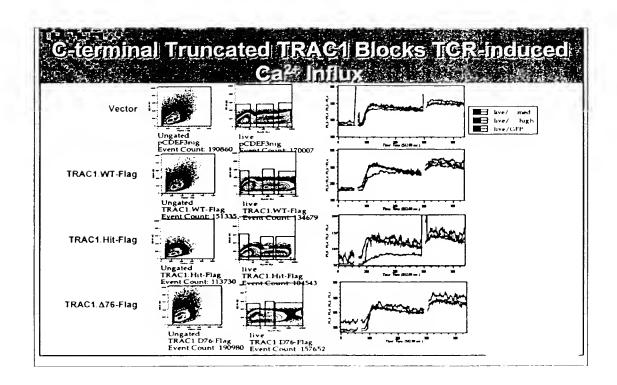


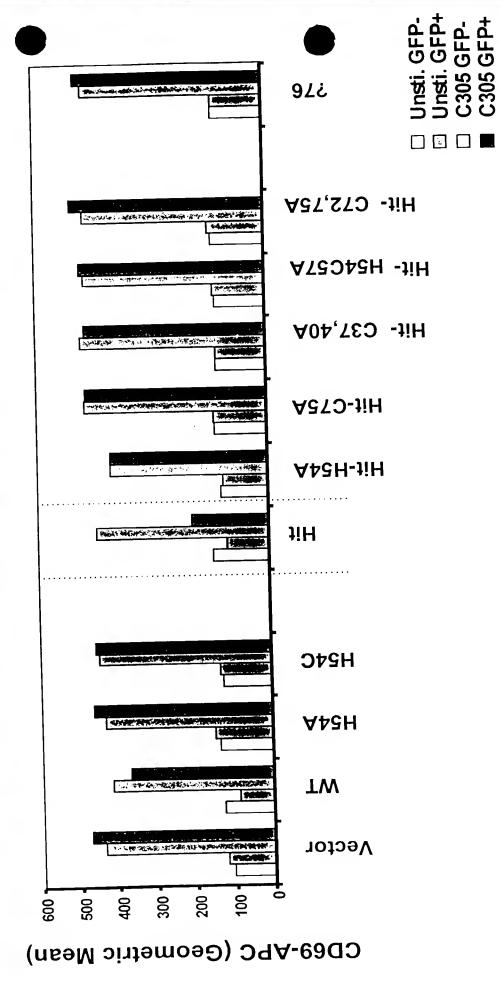




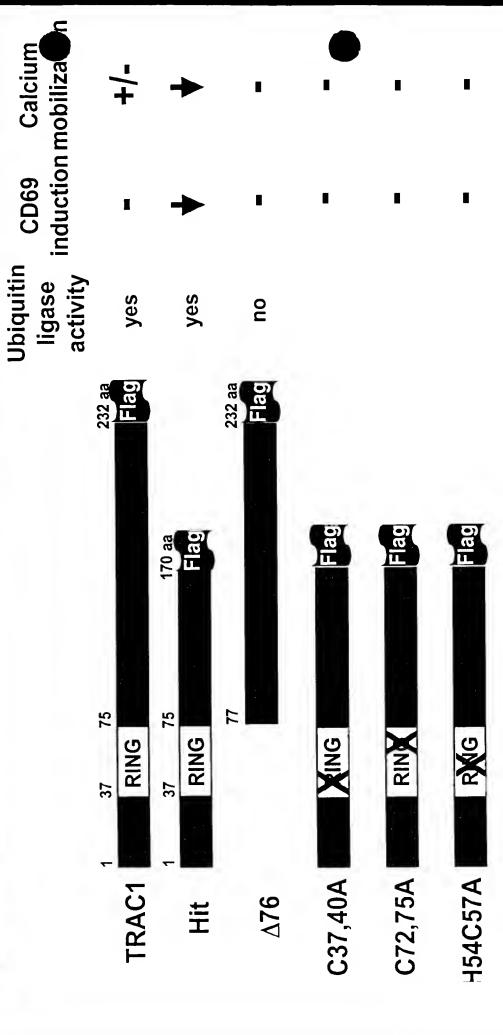
13B







Calcium



Cellular Lysate Transfected w/

pEF vector

pEF.TRAC1.WT

Purified E2s W/ His-tag

SHOON TROOF TO SHOOLH?

IN'-NPCH?

IN'-NPCH?

SPEGA!N

IN'-NPCH?

SPEGA!N

IN'-NPCH?

IN

← FLAG-TRAC1

17 — le Help

38

кDа

28 -

E2/TRAC1.tiff

